```
atg gca agt cca gag cac cct ggg agc cct ggc tgc atg gga ccc ata   48
Met Ala Ser Pro Glu His Pro Gly Ser Pro Gly Cys Met Gly Pro Ile
 1               5                  10                  15

acc cag tgc acg gca agg acc cag cag gaa gca cca gcc act ggc ccc   96
Thr Gln Cys Thr Ala Arg Thr Gln Gln Glu Ala Pro Ala Thr Gly Pro
            20                  25                  30

gac ctc ccg cac cca gga cct gac ggg cac tta gac aca cac agt ggc   144
Asp Leu Pro His Pro Gly Pro Asp Gly His Leu Asp Thr His Ser Gly
        35                  40                  45

ctg agc tcc aac tcc agc atg acc acg cgg gag ctt cag cag tac tgg   192
Leu Ser Ser Asn Ser Ser Met Thr Thr Arg Glu Leu Gln Gln Tyr Trp
    50                  55                  60

cag aac cag aaa tgc cgc tgg aag cac gtc aaa ctg ctc ttt gag atc   240
Gln Asn Gln Lys Cys Arg Trp Lys His Val Lys Leu Leu Phe Glu Ile
65                  70                  75                  80

gct tca gct cgc atc gag gag aga aaa gtc tct aag ttt gtg gtg tac   288
Ala Ser Ala Arg Ile Glu Glu Arg Lys Val Ser Lys Phe Val Val Tyr
                85                  90                  95

caa atc atc gtc atc cag act ggg agc ttt gac aac aac aag gcc gtc   336
Gln Ile Ile Val Ile Gln Thr Gly Ser Phe Asp Asn Asn Lys Ala Val
            100                 105                 110

ctg gaa cgg cgc tat tcc gac ttc gcg aag ctc cag aaa gcg ctg ctg   384
Leu Glu Arg Arg Tyr Ser Asp Phe Ala Lys Leu Gln Lys Ala Leu Leu
        115                 120                 125

aag acg ttc agg gag gag atc gaa gac gtg gag ttt ccc agg aag cac   432
Lys Thr Phe Arg Glu Glu Ile Glu Asp Val Glu Phe Pro Arg Lys His
    130                 135                 140

ctg act ggg aac ttc gct gag gag atg atc tgt gag cgt cgg cgc gcc   480
Leu Thr Gly Asn Phe Ala Glu Glu Met Ile Cys Glu Arg Arg Arg Ala
145                 150                 155                 160

ctg cag gag tac ctg ggc ctg ctc tac gcc atc cgc tgc gtg cgc cgc   528
Leu Gln Glu Tyr Leu Gly Leu Leu Tyr Ala Ile Arg Cys Val Arg Arg
                165                 170                 175

tcc cgg gag ttc ctg gac ttc ctc acg cgg ccg gag ctg cgc gag gct   576
Ser Arg Glu Phe Leu Asp Phe Leu Thr Arg Pro Glu Leu Arg Glu Ala
            180                 185                 190

ttc ggc tgc ctg cgg gcc ggc cag tac ccg cgc gcc ctg gag ctg ctg   624
Phe Gly Cys Leu Arg Ala Gly Gln Tyr Pro Arg Ala Leu Glu Leu Leu
        195                 200                 205

ctg cgc gtg ctg ccg ctg cag gag aag ctc acc gcc cac tgc cct gcg   672
Leu Arg Val Leu Pro Leu Gln Glu Lys Leu Thr Ala His Cys Pro Ala
    210                 215                 220

gcc gcc gtc ccg gcc ctg tgc gcc gtg ctg ctg tgc cac cgc gac ctc   720
Ala Ala Val Pro Ala Leu Cys Ala Val Leu Leu Cys His Arg Asp Leu
225                 230                 235                 240
```

FIGURE 1

```
gac cgc ccc gcc gag gcc ttc gcg gcc gga gag agg gcc ctg cag cgc     768
Asp Arg Pro Ala Glu Ala Phe Ala Ala Gly Glu Arg Ala Leu Gln Arg
                245                 250                 255

ctg cag gcc cgg gag ggc cat cgc tac tat gcg cct ctg ctg gac gcc     816
Leu Gln Ala Arg Glu Gly His Arg Tyr Tyr Ala Pro Leu Leu Asp Ala
            260                 265                 270

atg gtc cgc ctg gcc tac gcg ctg ggc aag gac ttc gtg act ctg cag     864
Met Val Arg Leu Ala Tyr Ala Leu Gly Lys Asp Phe Val Thr Leu Gln
        275                 280                 285

gag agg ctg gag gag agc cag ctc cgg agg ccc acg ccc cga ggc atc     912
Glu Arg Leu Glu Glu Ser Gln Leu Arg Arg Pro Thr Pro Arg Gly Ile
    290                 295                 300

acc ctg aag gag ctc act gtg cga gaa tac ctg cac tga                 951
Thr Leu Lys Glu Leu Thr Val Arg Glu Tyr Leu His
305                 310                 315
```

FIGURE 1 cont'd

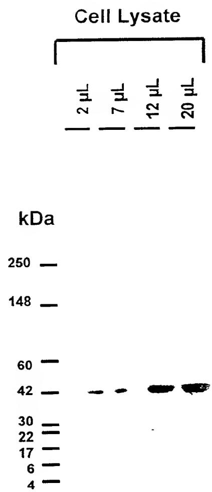

FIGURE 2

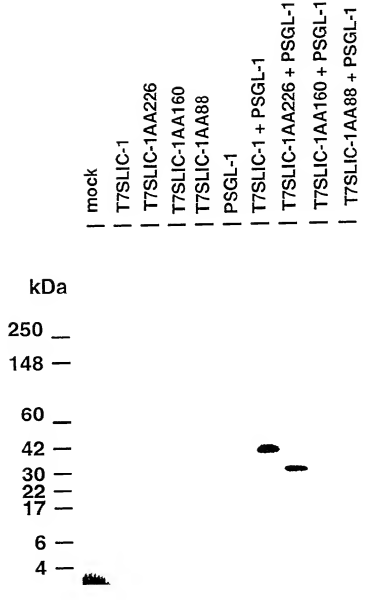
kDa
250
148
60
42
30
22
17
6
4
mock
T7SLIC-1
T7SLIC-1AA226
T7SLIC-1AA160
T7SLIC-1AA88
PSGL-1
T7SLIC-1 + PSGL-1
T7SLIC-1AA226 + PSGL-1
T7SLIC-1AA160 + PSGL-1
T7SLIC-1AA88 + PSGL-1

FIGURE 3

Genomic exon-intron boundary structure of the human SLIC-1 gene

```
Exon 1 - GAGACTGGAG -86                                          87-  CCTTGGAGCA - EXON 2
         ||||||||||                                                   ||||||||||
         GAGACTGGAGgtcagtattt ..... Intron 1 (3651bp) ..... cctctggcagCCTTGGAGCA

Exon 2 - CGGGCACTTA -224                                        225-  ACACACACAG - EXON 3
         ||||||||||                                                   ||||||||||
         CGGGCACTTAgtgggctt .....   Intron 2 (1474bp)  .....gtccttccagACACACACAG

Exon 3 - TAAGTTTGTG -377                                        378-  GTGTACCAAA - EXON 4
         ||||||||||                                                   ||||||||||
         TAAGTTTGTGgtaagcagag .....  Intron 3 (1695bp)  .....tgcgccctagGTGTACCAAA
```

Genomic exon-intron boundary structure of the mouse SLIC-1 gene

```
Exon 1 - TCCCAGGTCA                                                  CCTTGGAGCA - EXON 2
         ||||||||||                                                  ||||||||||
         TCCCAGGTCAgtcagtgttt..........  Intron 1 ........ gctcaggtagCCTTGGAGCA

Exon 2 - GGATCAGAAA                                                  CTCAGGTAGC - EXON 3
         ||||||||||                                                  ||||||||||
         GGATCAGAAAggtaaactgg..........  Intron 2 ......... ctcttgtagCTCAGGTAGC

Exon 3 - CAAGTTTGTG                                                  ATGTACCAAG - EXON 4
         ||||||||||                                                  ||||||||||
         CAAGTTTGTGgtaagcagag..........  Intron 3 ........ ctgcctgcagATGTACCAAG
```

FIGURE 4